

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 13, 2006, 18:37:13 ; Search time 167 Seconds
(without alignments)
950.749 Million cell updates/sec

Title: US-09-931-701A-2

Perfect score: 1901

Sequence: 1 MNKPLGKIVASTALISVAFA.....SLGSTMVYSGLVNAEAATR 380

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA Main:

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pap:*
2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pap:*
3: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pap:*
4: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pap:*
5: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pap:*
6: /cgn2_6/prodata/1/pubppa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1901	100.0	380	US-09-931-701-2	Sequence 2, Appl1
2	1777	93.5	380	US-10-324-152-8	Sequence 8, Appl1
3	1772	93.2	380	US-10-324-152-9	Sequence 9, Appl1
4	1770	93.1	380	US-09-824-893A-261	Sequence 261, App
5	1760	92.6	380	US-10-736-997-261	Sequence 261, App
6	1754.5	92.3	377	US-09-813-408-1	Sequence 2, Appl1
7	1750.5	92.3	380	US-10-476-463-4	Sequence 4, Appl1
8	1670.5	87.9	380	US-10-836-959-4	Sequence 4, Appl1
9	1667.5	87.7	380	US-10-836-959-2	Sequence 2, Appl1
10	1665.5	87.6	380	US-10-476-463-2	Sequence 2, Appl1
11	1664.5	87.6	380	US-10-836-959-6	Sequence 6, Appl1
12	1664.5	87.4	374	US-10-873-610-2	Sequence 2, Appl1
13	1490	78.4	374	US-09-813-408-6	Sequence 6, Appl1
14	1461.5	73.0	379	US-09-813-408-7	Sequence 7, Appl1
15	1387	75.9	382	US-09-813-408-7	Sequence 7, Appl1
16	1311.5	69.0	383	US-10-872-162-2	Sequence 2, Appl1
17	1303.5	68.6	383	US-10-872-162-2	Sequence 2, Appl1
18	1284	67.5	269	US-09-837-235-16	Sequence 16, Appl1
19	1284	67.5	269	US-10-336-324-4	Sequence 4, Appl1
20	1284	67.5	269	US-10-403-105-7	Sequence 7, Appl1
21	1284	67.5	269	US-11-043-731-16	Sequence 16, Appl1
22	1284	67.5	269	US-11-104-845-4	Sequence 4, Appl1
23	1280	67.3	268	US-10-873-917-5	Sequence 5, Appl1
24	1280	67.3	268	US-10-872-162-4	Sequence 4, Appl1
25	1279	67.3	269	US-08-332-678-10	Sequence 10, Appl1
26	1279	67.3	269	US-09-060-854B-6	Sequence 6, Appl1
27	1279	67.3	269	US-09-975-139-1	Sequence 1, Appl1

28	1279	67.3	269	US-09-976-414-8	Sequence 8, Appl1
29	1279	67.3	269	US-09-736-116-49	Sequence 49, Appl1
30	1279	67.3	269	US-09-957-806A-24	Sequence 24, Appl1
31	1279	67.3	269	US-09-957-806A-56	Sequence 56, Appl1
32	1279	67.3	269	US-10-075-907-1	Sequence 1, Appl1
33	1279	67.3	269	US-10-075-895-1	Sequence 1, Appl1
34	1279	67.3	269	US-10-033-325-6	Sequence 6, Appl1
35	1279	67.3	269	US-10-209-812-3	Sequence 3, Appl1
36	1279	67.3	269	US-10-104-693-4	Sequence 4, Appl1
37	1279	67.3	269	US-10-228-572-6	Sequence 6, Appl1
38	1279	67.3	269	US-10-324-152-5	Sequence 5, Appl1
39	1279	67.3	269	US-10-242-549-5	Sequence 5, Appl1
40	1279	67.3	269	US-10-313-853-1	Sequence 1, Appl1
41	1279	67.3	269	US-10-336-324-7	Sequence 7, Appl1
42	1279	67.3	269	US-10-403-105-10	Sequence 10, Appl1
43	1279	67.3	269	US-10-243-576-5	Sequence 5, Appl1
44	1279	67.3	269	US-10-423-649-6	Sequence 6, Appl1
45	1279	67.3	269	US-10-323-324-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1					
US-09-931-701-2					
Sequence 2, Application US/09931701					
Publication No. US20040241820A1					
GENERAL INFORMATION:					
APPLICANT: Outtrup, Helle					
APPLICANT: Pedersen, Poul					
APPLICANT: Sorensen, Marianne					
TITLE OF INVENTION: Subtilase Enzymes					
FILE REFERENCE: 10065.200-US					
CURRENT APPLICATION NUMBER: US/09/931,701					
CURRENT FILING DATE: 2001-08-16					
NUMBER OF SEQ ID NOS: 9					
SOFTWARE: PatentIn version 3.1					
SEQ ID NO 2					
LENGTH: 380					
TYPE: PRT					
ORGANISM: Bacillus clausii					
US-09-931-701-2					
Query Match					
Best Local Similarity 100.0%; Score 1901; DB 3; Length 380;					
Best Local Similarity 100.0%; Pred No. 7.6e-138;					
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MNKP	L	GKIVASTALISVAFASSSSIASAAEAK	EKKYLGNEQEAASEFYEOVDANNDAV 60
DB	1	MNKP	L	GKIVASTALISVAFASSSSIASAAEAK	EKKYLGNEQEAASEFYEOVDANNDAV 60
QY	61	LS	EE	EEVEIEELHFEFTIVLSVLSPEVDLT	LEDPALSYIEEDVEVIMQSVWGIS 120
DB	61	LS	EE	EEVEIEELHFEFTIVLSVLSPEVDLT	LEDPALSYIEEDVEVIMQSVWGIS 120
QY	121	RV	Q	APAAHRCGTGSGVKAVLDTGISAP	DLNIRGSAFVNGEPTVQDNGHGTAVGT 180
DB	121	RV	Q	APAAHRCGTGSGVKAVLDTGISAP	DLNIRGSAFVNGEPTVQDNGHGTAVGT 180
QY	181	IA	L	ANNSIGLVAPAAELVAVKVLAA	NGRPVSSIAQGLEMANNGMDVANISLSGSP 240
DB	181	IA	L	ANNSIGLVAPAAELVAVKVLAA	NGRPVSSIAQGLEMANNGMDVANISLSGSP 240
QY	241	SAT	L	EOAVNSATSRGLVVAATGNSGT	SLDYPARYANMAVAGATDQNNRASFQYAG 300
DB	241	SAT	L	EOAVNSATSRGLVVAATGNSGT	SLDYPARYANMAVAGATDQNNRASFQYAG 300
QY	301	LD	I	VAGVAVQSTYPSGTASRNGT	SMATPRHVGVAAVYKQKPSNSNOIRHKLKNTAT 360
DB	301	LD	I	VAGVAVQSTYPSGTASRNGT	SMATPRHVGVAAVYKQKPSNSNOIRHKLKNTAT 360
QY	361	SL	G	STMVYSGLVNAEAATR 380	
DB	361	SL	G	STMVYSGLVNAEAATR 380	

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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:37:57 ; Search time 23 Seconds

(without alignments)
459.881 Million cell updates/sec

Title: US-09-931-701A-2

Perfect score: 1901

Sequence: 1 MNKPLGKIVASTALLISVAF.....SLGSTNLXGSGLVNAEAATR 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 16167 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 16167

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubppa/ECT_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1279	67.3	269	US-11-020-602-6	Sequence 6, Appl1
2	972.5	51.2	272	US-11-020-602-236	Sequence 236, App
3	914	48.1	382	US-11-020-602-2	Sequence 2, Appl1
4	898.5	47.3	379	US-11-156-062-23	Sequence 23, Appl1
5	849	44.7	275	US-11-020-602-4	Sequence 4, Appl1
6	835	43.9	275	US-11-065-943-54	Sequence 54, Appl1
7	835	43.9	275	US-11-020-602-3	Sequence 3, Appl1
8	815.5	42.9	274	US-11-156-062-14	Sequence 14, Appl1
9	815.5	42.9	274	US-11-156-062-16	Sequence 16, Appl1
10	814.5	42.8	274	US-11-020-602-5	Sequence 5, Appl1
11	810.5	42.6	274	US-11-156-062-10	Sequence 4, Appl1
12	809.5	42.6	274	US-11-156-062-12	Sequence 12, Appl1
13	809.5	42.6	274	US-11-156-062-18	Sequence 18, Appl1
14	809.5	42.6	274	US-11-156-062-2	Sequence 2, Appl1
15	804.5	42.3	274	US-11-156-062-2	Sequence 6, Appl1
16	804.5	42.3	274	US-11-156-062-6	Sequence 6, Appl1
17	803.5	42.3	274	US-11-156-062-8	Sequence 8, Appl1
18	609.5	32.1	591	US-10-510-386-22	Sequence 22, Appl1
19	410	21.6	874	US-10-510-386-28	Sequence 28, Appl1
20	410	21.6	1067	US-10-510-386-200	Sequence 200, App
21	355	18.7	802	US-10-510-386-2	Sequence 2, Appl1
22	354	18.6	1432	US-10-510-386-218	Sequence 218, App
23	290	15.3	1052	US-11-020-602-208	Sequence 208, App
24	280.5	14.8	280	US-11-020-602-209	Sequence 209, App
25	234	12.3	49	US-11-011-666-12	Sequence 12, Appl1

26	222	11.7	51	7	US-11-011-666-9	Sequence 9, Appl1
27	222	11.7	740	7	US-11-036-568A-24714	Sequence 24714, A
28	222	11.7	777	7	US-11-036-568A-24713	Sequence 24713, A
29	222	11.7	790	7	US-11-036-568A-24712	Sequence 24712, A
30	222	11.7	969	6	US-10-501-035-361	Sequence 361, App
31	221	11.6	48	7	US-11-011-666-8	Sequence 8, Appl1
32	211.5	11.1	759	7	US-11-036-568A-24027	Sequence 24027, A
33	211.5	11.1	764	7	US-11-036-568A-24026	Sequence 24026, A
34	210	11.0	794	7	US-11-218-986-2	Sequence 2, Appl1
35	210	11.0	820	6	US-10-821-234-1176	Sequence 1176, Ap
36	209	11.0	733	7	US-11-036-568A-24028	Sequence 24028, A
37	205.5	10.8	791	7	US-11-036-568A-31251	Sequence 31251, A
38	203	10.7	757	7	US-11-036-568A-31862	Sequence 31862, A
39	203	10.7	798	7	US-11-036-568A-31861	Sequence 31861, A
40	200.5	10.5	1647	7	US-11-052-554A-260	Sequence 260, App
41	193.5	10.2	755	7	US-11-037-243-82	Sequence 82, Appl1
42	192.5	10.1	722	7	US-11-036-568A-31863	Sequence 31863, A
43	190	10.0	672	7	US-11-036-568A-23983	Sequence 23983, A
44	190	10.0	680	7	US-11-036-568A-23982	Sequence 23982, A
45	187.5	9.9	470	6	US-10-873-528-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-11-020-602-6
Sequence 6, Application US/11020602
Publication No. US2006002464A1
GENERAL INFORMATION:
APPLICANT: Bette, David
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GCS2762
CURRENT APPLICATION NUMBER: US/11/020,602
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 269
TYPE: PRT
ORGANISM: Bacillus lentus
US-11-020-602-6

Query Match 67.3% Score 1279; DB 7; Length 269;
Best Local Similarity 93.3% Pred. No. 5.7e-85;
Matches 251; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
112 AQSVMGISRQVAPAAHNRGVTSQVAVLDGTGISHAPDLNIRGASFTGPTQDN 171
1 AQSVMGISRQVAPAAHNRGVTSQVAVLDGTGISHAPDLNIRGASFTGPTQDN 60
172 GGHVAVAGTIALNNSIGLVAPAAELVAVLANGRPVSSIAQGLEMAAGNMDDVA 231
61 GGHVAVAGTIALNNSIGLVAPAAELVAVLANGRPVSSIAQGLEMAAGNMDDVA 120
223 NLSLSPSPSATLEQAVNSATSRGLVVAATNSGSGLDYEPARYANMAVAGATDONNR 291
121 NLSLSPSPSATLEQAVNSATSRGLVVAATNSGSGLDYEPARYANMAVAGATDONNR 180
292 ASFSQYGAAGLDIVAGVNVQSTYPSSTYASFGNSTMATPHVAVVALVKKPKPSMSVQI 351
181 ASFSQYGAAGLDIVAGVNVQSTYPSSTYASFGNSTMATPHVAVVALVKKPKPSMSVQI 240
352 RNLKQVATSLGSLTSLVYSGGLVNAEAATR 380
241 RNLKQVATSLGSLTSLVYSGGLVNAEAATR 269

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OM protein - protein search, using SW model

Run on: March 13, 2006, 18:25:57 ; Search time 48 Seconds
(without alignments)
654,516 Million cell updates/sec

Title: US-09-931-701a-2

Perfect score: 1901

Sequence: 1 MNKPLGKIVASTALLISVA.....SLGSTNYGSGVNAEATR 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
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2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/prodata/1/1aa/7 COMB.pep.*
4: /cgn2_6/prodata/1/1aa/8 COMB.pep.*
5: /cgn2_6/prodata/1/1aa/9 COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1777	93.5	380	2	US-09-049-867-2
2	1777	93.5	380	2	US-08-269-050-2
3	1777	93.5	380	6	5217878-2
4	1777	93.5	380	6	5336611-2
5	1772	93.2	380	1	US-07-918-318-2
6	1772	93.2	380	1	US-08-413-724-2
7	1772	93.2	380	2	US-08-853-494-2
8	1772	93.2	380	2	US-08-716-293-1
9	1772	93.2	380	2	US-09-445-270-7
10	1770	93.1	380	2	US-09-824-893A-261
11	1758	92.5	380	2	US-09-445-270-9
12	1618	85.1	349	1	US-07-661-378A-2
13	1491	78.4	378	1	US-07-772-087-3
14	1284	67.5	269	1	US-08-431-387-6
15	1284	67.5	269	2	US-08-269-050-4
16	1284	67.5	269	2	US-08-090-207-1
17	1284	67.5	269	2	US-09-512-251A-4
18	1284	67.5	269	2	US-09-515-150A-4
19	1284	67.5	269	2	US-09-196-281-7
20	1284	67.5	269	2	US-10-336-324-4
21	1284	67.4	269	6	5217878-3
22	1284	67.4	269	1	US-07-706-691G-16
23	1282	67.4	269	1	US-08-254-021-16
24	1282	67.4	269	1	US-08-618-446-16
25	1282	67.4	269	1	US-08-980-135-16
26	1282	67.4	269	2	US-09-585-798-16
27	1279	67.3	269	1	US-07-706-691G-31

28	1279	67.3	269	1	US-08-254-021-31	Sequence 31, App1
29	1279	67.3	269	1	US-08-431-387-5	Sequence 5, App1
30	1279	67.3	269	1	US-08-322-677A-10	Sequence 10, App1
31	1279	67.3	269	1	US-08-322-676-10	Sequence 10, App1
32	1279	67.3	269	1	US-08-140-083A-10	Sequence 10, App1
33	1279	67.3	269	1	US-08-618-446-31	Sequence 31, App1
34	1279	67.3	269	2	US-08-898-218-10	Sequence 10, App1
35	1279	67.3	269	2	US-08-848-793-10	Sequence 10, App1
36	1279	67.3	269	2	US-09-980-135-31	Sequence 31, App1
37	1279	67.3	269	2	US-09-255-502-5	Sequence 5, App1
38	1279	67.3	269	2	US-09-024-532-3	Sequence 3, App1
39	1279	67.3	269	2	US-08-090-207-2	Sequence 2, App1
40	1279	67.3	269	2	US-09-178-155-6	Sequence 6, App1
41	1279	67.3	269	2	US-09-445-270-5	Sequence 5, App1
42	1279	67.3	269	2	US-09-467-536A-1	Sequence 1, App1
43	1279	67.3	269	2	US-09-234-957-1	Sequence 1, App1
44	1279	67.3	269	2	US-09-585-798-31	Sequence 31, App1
45	1279	67.3	269	2	US-09-417-359A-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
US-09-049-867-2
; Sequence 2, Application US/09049867
; Patent No. 6124097

GENERAL INFORMATION:

APPLICANT: Van Eekelen, Christiaan A.G.

APPLICANT: Van Der Laan, Johannes C.

APPLICANT: Mulleners, Leo J.S.M.

TITLE OF INVENTION: Stable Gene Amplification in

TITLE OF INVENTION: Chromosomal DNA of Prokaryotic Microorganisms

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSES: McDonnell Boehnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,867

FILING DATE: 27-MAR-1998

CLASSIFICATION:

APPLICATION NUMBER: 08/295,082

FILING DATE: 24-AUG-94

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-049-867-2

Query Match

Best Local Similarity 93.5%; Score 1777; DB 2; Length 380;

Matches 354; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 MNKPLGKIVASTALLISVAFFSSSIASAEAEKTLIGNEQAVSEFTEQVANDVAV 60

DB 1 MNKPLGKIVASTALLISVAFFSSSIASAEAEKTLIGNEQAVSEFTEQVANDVAV 60

QY 61 LSEBREVETELHEBETIPVLSVELSPEDVDLELDPALSYIEEDVETIMOSVWGIS 120

DB 61 LSEBREVETELHEBETIPVLSVELSPEDVDLELDPALSYIEEDVETIMOSVWGIS 120

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 13, 2006, 18:18:46 ; Search time 224 Seconds

(without alignment)
1196.878 Million cell updates/sec

Title: US-09-931-701a-2

Sequence: 1 MKKPKAKIVASTALLISVAF.....SLGSTNLVGGSLVNEAATR 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1777	93.5	380	1 ELYA_BACAO	P27693 bacillus a1
2	1772	93.2	380	1 ELYA_BACCS	P41362 bacillus c1
3	1768	93.0	380	1 PRTW_BACSK	Q99405 bacillus c1
4	1500.5	78.9	379	2 O66153_BACSP	O66153 bacillus sp
5	1494	78.6	378	1 ELYA_BACYA	P20774 bacillus sp
6	1387	73.0	382	2 O45522_9BACT	O45522 bacillus sp
7	1279	67.3	269	1 SUBS_BACLE	P29600 bacillus sp
8	1278	67.2	269	1 SUBS_BACLE	P29599 bacillus le
9	1041.5	54.8	361	2 O45521_BACSP	O45521 bacillus sp
10	1037.5	54.6	361	1 ELYA_BACHD	P41363 bacillus ha
11	978.5	51.5	374	2 O45523_BACSP	O45523 bacillus sp
12	976.5	51.4	378	2 O45466_BACSP	O45466 bacillus sp
13	974	51.2	376	2 O76KL9_9BACT	O76KL9 bacillus sp
14	949.5	49.9	381	2 O586F0_BACSU	O586F0 bacillus su
15	945.5	49.7	381	2 O847A2_BACSU	O847A2 bacillus su
16	942.5	49.6	381	1 SUBN_BACNA	P35835 bacillus su
17	942.5	49.6	381	2 O548F3_BACNA	O548F3 bacillus su
18	940.5	49.5	381	2 O84F18_BACSU	O84F18 bacillus su
19	937.5	49.3	381	1 SUBT_BACSA	P08171 bacillus su
20	937.5	49.3	381	1 O581V1_BACSU	O581V1 bacillus su
21	934.5	49.2	381	1 SUBT_BACST	P04189 bacillus su
22	933.5	49.1	381	1 SUBT_BACST	P29142 bacillus su
23	933.5	49.0	381	2 O581U9_BACSU	O581U9 bacillus su
24	932	49.0	382	1 SUBT_BACAM	P00782 bacillus su
25	930	48.9	382	2 O5XZF9_9BACL	O5XZF9 bacillus su
26	928.5	48.8	362	2 O5EF09_BACNA	O5EF09 bacillus su
27	926	48.7	382	2 O61T79_9BACT	O61T79 bacillus su
28	920.5	48.4	381	2 O7WVAG_BACSU	O7WVAG bacillus su
29	918.5	48.3	377	2 O6L9T7_9BACT	O6L9T7 bacillus su
30	918.5	48.3	379	2 O9FDF4_BACLI	O9FDF4 bacillus li
31	918.5	48.3	379	2 O6SLP7_BACLD	O6SLP7 bacillus li

32	913	48.0	382	2 O87655_BACSU	O87655 bacillus su
33	910	47.9	382	2 O5UKQ4_9BACT	O5UKQ4 bacillus sp
34	909.5	47.8	379	1 SUBT_BACLI	P00780 bacillus li
35	909.5	47.8	379	2 O45467_BACSP	O45467 bacillus sp
36	898.5	47.3	379	2 O6PNN5_BACLI	O6PNN5 bacillus li
37	894.5	47.1	379	2 O53521_BACLI	O53521 bacillus li
38	894.5	47.1	379	2 O6BGN9_BACMO	O6BGN9 bacillus mo
39	894.5	47.1	379	2 O4PKR6_BACLI	O4PKR6 bacillus li
40	885.5	46.6	374	2 O9F942_BACLI	O9F942 bacillus li
41	885.5	46.6	374	2 O9F941_BACLI	O9F941 bacillus li
42	883	46.4	404	2 O76L29_9BACT	O76L29 bacillus sp
43	881.5	46.4	374	2 O9F943_BACLI	O9F943 bacillus li
44	878	46.2	379	2 O45301_BACLI	O45301 bacillus li
45	867.5	45.6	310	2 O9FDF3_BACLI	O9FDF3 bacillus li

ALIGNMENTS

RESULT 1

ID	ELYA_BACAO	STANDARD	PRT	380 AA.
AC	P27693			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Alkaline protease precursor (EC 3.4.21.-)			
OS	Bacillus alcalophilus			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus			
OX	NCBI_TaxID=1445			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE			
RC	STRAIN=PB92			
RX	MEDLINE=91282483; PubMed=2059048			
RA	van der Laan J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset O., Mulleners L.J.M., Dijkstra B.W.;			
RT	"Crystall structure of the high-alkaline serine protease PB92 from Bacillus alcalophilus."			
RL	Protein Eng. 5:405-411(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS)			
RX	MEDLINE=92390330; PubMed=1518768			
RA	van der Laan J.C., Teplyakov A.V., Kelders H., Kalk K.H., Misset O., Mulleners L.J.M., Dijkstra B.W.;			
RT	"X-ray structure determination and comparison of two crystal forms of a variant (Asn15arg) of the alkaline protease from Bacillus alcalophilus refined at 1.85-A resolution."			
RL	J. Mol. Biol. 228:108-117(1992).			
RN	[4]			
RP	STRUCTURE BY NMR OF 112-380.			
RC	STRAIN=PB92			
RX	MEDLINE=92727237; PubMed=9115441; DOI=10.1016/S0969-2126(97)00208-6			
RA	Martini J.R., Mulder F.A., Karim-Nejad Y., van der Zwan J., Martini M., Schipper D., Boelens R.;			
RT	"The solution structure of serine protease PB92 from Bacillus alcalophilus presents a rigid fold with a flexible substrate-binding site."			
RL	Structure 5:521-532(1997).			
CC	-1-COPFACTOR: Binds 2 calcium ions per subunit.			
CC	-1-SUBCELLULAR LOCATION: Secreted.			
CC	-1-SIMILARITY: Belongs to the peptidase 58 family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its			

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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:18:21 / Search time 189 seconds
(without alignments)
883.407 Million cell updates/sec

Title: US-09-931-701A-2

Perfect score: 1901

Sequence: 1 MNKPLKIVASTALITVAF.....SLGSTNYGSGLVNAEAATR 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: A_Geneseq_21.*
2: geneseqdp1980s.*
3: geneseqdp1990s.*
4: geneseqdp2000s.*
5: geneseqdp2001s.*
6: geneseqdp2002s.*
7: geneseqdp2003s.*
8: geneseqdp2004s.*
9: geneseqdp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1901	100.0	380	5 AAU78181	AAU78181 B. clausi
2	1777	93.5	380	1 AAP80867	AAP80867 Sequence
3	1777	93.5	380	1 AAP90915	AAP90915 P92 Ser1
4	1777	93.5	380	2 AAR43046	AAR43046 Wild-type
5	1777	93.5	380	4 AAB82790	AAB82790 Bacillus
6	1777	93.5	380	5 AAB16857	AAB16857 Bacillus
7	1777	93.5	380	7 ADE81100	ADE81100 Bacillus
8	1777	93.2	380	2 AAR10892	AAR10892 B. alcalop
9	1777	93.2	380	2 AAR27131	AAR27131 Stabillise
10	1777	93.2	380	2 AAR56514	AAR56514 High alka
11	1777	93.2	380	2 AAR73777	AAR73777 Bacillus
12	1777	93.2	380	2 AAM82797	AAM82797 B. lentus
13	1777	93.2	380	3 AAY7004	AAY7004 Bacillus
14	1777	93.2	380	3 AAB83776	AAB83776 Subtilisi
15	1777	93.2	380	7 ADE81101	ADE81101 Bacillus
16	1777	93.2	380	8 ADJ46880	ADJ46880 B. lentus
17	1777	93.1	380	4 AAU38874	AAU38874 Subtilisi
18	1768	93.1	380	2 AAR31928	AAR31928 High alka
19	1768	93.0	380	2 AAR64214	AAR64214 Alkaline
20	1768	93.0	380	2 AAR94075	AAR94075 Bacillus
21	1768	93.0	380	2 AAR94080	AAR94080 Bacillus
22	1767	93.0	380	2 AAR34611	AAR34611 High alka
23	1767	93.0	380	2 AAR94081	AAR94081 Bacillus
24	1766	92.9	380	2 AAR11189	AAR11189 Pre-pro a

25	1766	92.9	380	2 AAR34610	AAR34610 High alka
26	1766	92.9	380	2 AAR75163	AAR75163 B. lentus
27	1766	92.9	380	2 AAR94076	AAR94076 Bacillus
28	1766	92.9	380	2 AAR94077	AAR94077 Bacillus
29	1766	92.9	380	2 AAR94083	AAR94083 Bacillus
30	1766	92.9	380	2 AAR94078	AAR94078 Bacillus
31	1766	92.9	380	2 AAR94079	AAR94079 Bacillus
32	1766	92.9	380	2 AAR34891	AAR34891 Preferred
33	1766	92.9	380	2 AAW34774	AAW34774 Preferred
34	1766	92.9	380	3 AAY77005	AAY77005 Bacillus
35	1766	92.9	380	3 AAB03777	AAB03777 Subtilisi
36	1766	92.9	380	8 ADJ46881	ADJ46881 B. lentus
37	1765	92.8	380	2 AAR34615	AAR34615 High alka
38	1765	92.8	380	2 AAR34605	AAR34605 High alka
39	1764	92.8	380	2 AAR34612	AAR34612 High alka
40	1764	92.8	380	2 AAR94082	AAR94082 Bacillus
41	1763	92.7	380	2 AAR34618	AAR34618 High alka
42	1763	92.7	380	2 AAR34613	AAR34613 High alka
43	1763	92.7	380	2 AAR34614	AAR34614 High alka
44	1763	92.7	380	2 AAR34617	AAR34617 High alka
45	1763	92.7	380	2 AAR34620	AAR34620 High alka

ALIGNMENTS

RESULT 1	AAU78181	standard; protein; 380 AA.
ID	AAU78181	
XX	AAU78181;	
AC	29-AUG-2003 (revised)	
DT	05-JUN-2002 (first entry)	
XX	B. clausi subtilase.	
DE	Subtilase; detergent; laundry; dishwasher; egg stain removal.	
XX	Bacillus clausii; strain HSB10.	
OS		
XX	Key	Location/Qualifiers
FX	Peptide	1..111
FT	Protein	/label=Signal_peptide
FT		112..380
FT		/label=Mature_subtilase
XX		
PN	WO200216547-A2.	
XX		
PD	26-FEB-2002.	
XX		
PF	21-AUG-2001; 2001WO-DK000551.	
XX		
PR	21-AUG-2000; 2000DK-00001232.	
XX		
PA	(NOVO) NOVOZYMES AS.	
XX		
PI	Outtrup H, Pedersen PE, Sorensen MV;	
XX		
DR	WPI; 2002-280919/32.	
XX		
PT	N-PSDB; ABR12132.	
XX		
PT	Novel subtilase enzyme that exhibits low inhibition by substances present	
XX	in eggs such as trypsin inhibitor type IV-0, useful in a cleaning or	
XX	detergent composition and for removal of egg stains.	
PS	Claim 3; Page 87-88; 88pp; English.	
XX		
CC	The invention relates a subtilase enzyme and its encoding nucleic acid	
CC	(or a protein 95 % similar to the subtilase). Also included are a	
CC	construct comprising the nucleic acid operably linked to one or more	
CC	control sequences capable of directing the expression of the subtilase in	
CC	a suitable host, a recombinant expression vector comprising the construct	

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OW protein - protein search, using sw model

Run on: March 13, 2006, 18:22:07 ; Search time 41 Seconds

(without alignments)
891.765 Million cell updates/sec

Title: US-09-931-701a-2

Perfect score: 1901
Sequence: 1 MNKPLGKIVASFTALLISVAF.....SLGSTNLYGSLVNAEAATR 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1777	93.5	380	2 A49778	high-alkaline seri
2	1494	78.6	378	2 A33573	high-alkaline seri
3	1387	73.0	382	2 I39780	subtilisin (EC 3.4
4	1044.5	54.9	361	2 A48373	high-alkaline seri
5	1037.5	54.6	361	2 G83756	subtilisin-type al
6	978.5	51.5	374	2 I39781	subtilisin (EC 3.4
7	942.5	49.6	381	2 JH0778	subtilisin (EC 3.4
8	938.5	49.4	381	1 SUBSI	subtilisin (EC 3.4
9	937.5	49.3	381	1 SUBSI	subtilisin (EC 3.4
10	933.5	49.1	381	1 JQ1487	subtilisin (EC 3.4
11	932	49.0	382	1 SUBSN	subtilisin (EC 3.4
12	909.5	47.8	379	1 SUBSC	subtilisin (EC 3.4
13	843	44.3	272	2 A23624	subtilisin (EC 3.4
14	821.5	43.2	372	2 D83735	subtilisin-type al
15	811.5	42.7	275	2 JCL085	subtilisin (EC 3.4
16	796.5	41.9	274	1 SUBSD	subtilisin (EC 3.4
17	681.5	35.8	645	1 SUBSM	serine proteinase
18	642.5	33.8	397	2 JH0778	cysteine-dependent
19	618	32.5	384	2 JQ1487	alkaline proteinase
20	603	31.7	279	1 JCM402	thermolase (EC 3.4
21	559.5	29.4	436	2 I39973	alkaline serine pr
22	553.5	29.1	401	2 I39974	serine proteinase
23	553.5	29.1	525	2 G8406	halolysin (importe
24	539	28.4	792	2 H83736	subtilisin-type al
25	534	28.1	440	2 H72784	probable alkaline
26	528.5	27.8	488	2 A11930	proteinase (import
27	519.5	27.3	613	2 S75976	hypothetical prote
28	514.5	27.1	326	1 C41335	microbial serine p
29	512	26.9	580	2 S11890	serine proteinase

30	510.5	26.9	588	2 C83836	subtilisin-type pr
31	494.5	26.0	534	1 J50173	alkaline proteinase
32	489	25.7	519	2 S71451	halolysin R4 (EC 3
33	485	25.5	615	2 AH2248	proteinase (import
34	482.5	25.4	401	2 A57690	aerolysin precursor
35	482	25.4	419	1 S25835	subtilisin (EC 3.4
36	481.5	25.3	321	1 S27501	alkaline proteinase
37	480	25.2	513	1 A35742	aqualysin (EC 3.4
38	479.5	25.2	319	2 I39866	microbial serine p
39	477.5	25.1	420	1 S23407	subtilisin (EC 3.4
40	473	24.9	535	2 B82358	alkaline serine pr
41	462.5	24.3	1052	2 H83909	cell wall-associat
42	457.5	24.1	591	2 A75474	serine proteinase
43	456.5	24.0	1448	2 A12007	Subtilase family P
44	452.5	23.8	322	2 G83922	intracellular alka
45	447	23.5	387	2 S11985	serine proteinase

ALIGNMENTS

RESULT 1

A49778 high-alkaline serine proteinase (EC 3.4.21.-) precursor - Bacillus alcalophilus (strai
N/Alternate names: subtilisin homolog, high-alkaline
C/Species: Bacillus alcalophilus
C/Date: 12-Mar-1994 #sequence_revision 24-Feb-1995 #text_change 05-Oct-2004
C/Accession: A49778; JCI244
R/van der Laan, J.C.; Gerritse, G.; Mulleners, L.J.S.M.; van der Hoek, R.A.C.; Quax, W
Appl. Environ. Microbiol. 57, 901-909, 1991
A/Title: Cloning, characterization, and multiple chromosomal integration of a Bacillus
A/Reference number: A49778; MUID:91282483; PMID:2059048
A/Accession: A49778

A/Molecule type: DNA

A/Residues: 1-380 <VNA>

A/Cross-references: UNIPROT:P27693; UNIPARC:UPI000002BADA; GB:M65086; NID:9142456; PIC
A/Experimental source: strain P892, ATCC 31408

A/Note: amino end of mature protein confirmed by peptide sequencing

R/Takami, H.; Kobayashi, T.; Kobayashi, M.; Yamamoto, M.; Nakamura, S.; Aono, R.; Hori
Biosci. Biotechnol. Biochem. 56, 1455-1460, 1992

A/Title: Molecular cloning, nucleotide sequence, and expression of the structural gene
A/Reference number: JCI244; MUID:93043753; PMID:1368952

A/Accession: JCI244

A/Molecule type: DNA

A/Residues: 1-195, 'S', 197-380 <TRK>

A/Cross-references: UNIPARC:UPI000002CPSA; GB:D13157; NID:9216231; PIDN:BA02442.1; PI

A/Experimental source: Bacillus alcalophilus Veddler, ATCC 21522 (Bacillus sp. 221)

C/Superfamily: Subtilisin; subtilisin homolog

C/Keywords: hydrolase; serine proteinase; zymogen

F1-27/Domain: signal sequence #status predicted <Sig>

F128-111/Domain: activation peptide #status predicted <PRO>

F112-380/Product: alkaline serine proteinase #status predicted <MAT>

F134-340/Domain: subtilisin homolog <SBT>

F143.173/Active site: Asp, His, Ser #status predicted

Query Match 93.5%; Score 1777; DB 2; Length 380;

Best Local Similarity 93.2%; Pred No. 1.6e-107;

Matches 354; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY	1 MNKPLGKIVASFTALLISVAFSSSIASAEAEKYLIGNEQEAASEFVEQVANDAV 60		
DB	1 MNKPLGKIVASFTALLISVAFSSSIASAEAEKYLIGNEQEAASEFVEQVANDAV 60		
QY	61 LSEEEVEIELEHEPFTIVLSVEISPEVDLTLEDPASISYEEDVEIMOSVWGS 120		
DB	61 LSEEEVEIELEHEPFTIVLSVEISPEVDLTLEDPASISYEEDVEIMOSVWGS 120		
QY	121 RVOAPAAHNRGVTSQVAVADTGISAPDINIRGASFFVGEPTQDNGHGTVAAGT 180		
DB	121 RVOAPAAHNRGVTSQVAVADTGISAPDINIRGASFFVGEPTQDNGHGTVAAGT 180		
QY	181 IAAIINISIGLVAPNAELIYAVKVLAAANGRPVSSIAQGLEAANGNGDVANISLQSPSP 240		
DB	181 IAAIINISIGLVAPNAELIYAVKVLAAANGRPVSSIAQGLEAANGNGDVANISLQSPSP 240		